## REMARKS

Claims 1-11, 13-14, 17-18, 21, 24, and 26-27 are currently under consideration. The claims have been amended to more particularly and distinctly claim the invention. No new mater is added.

### A. Claim Objections

Claims 1-11, 13, 14, 17, 21, 24, 26, and 27 are objected to by the Examiner. For consistency among the claims the Examiner has proposed the following amendments: "a specific antibody" of claim 1, line 10 should read "a specific antibody or fragment thereof" or "specific antibodies or fragments thereof", "antibody" of claim 13, lines 2, 4, and 5; claim 14, line 2; claim 17, line 2 should read "antibodies or fragments thereof" or "antibody or fragment thereof" (plural or singular where appropriate), "peptides" of claim 14, line 3 should read "proteins or peptides", and "peptides, or protein or peptide fragments" of claim 21, line 2 and claim 24, line 2 should read "proteins, peptides, protein fragments, or peptide fragments".

Applicant has amended the claims as proposed by the Examiner, therefore, the objections to the claims should be withdrawn.

### B. The Claims Satisfy the Written Description Requirement

Claims 1-11, 13, 14, 17, 21, 24, 26, and 27 rejected under 35 U.S.C. §112, first paragraph, as failing to comply with the written description requirement. According to the Examiner, the claims contain subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor, at the time the application was filed, had possession of the claimed invention. The Examiner maintains that Applicant has not provided support for the amendments received on August 9, 2011 particularly for the amendments requiring "all" proteins, peptides, protein fragments, or peptide fragments to be characterized and "those proteins, peptides, protein fragments, or peptide fragments binding to a specific antibody represent a heterogeneous class".

In this regard, the Examiner's attention is directed to [0048] of the specification which states that 100 % of the proteins, peptides, protein fragments or peptide fragements in the sample are characterized. Additionally, [0016] defines that the proteins, peptides, protein fragments or peptide fragments making up one heterogenous class all bind to the same molecule.

In view of the above, Applicant respectfully request withdrawal of the rejections under §112.

## C. The Claims are Definite

Claims 1-11, 13, 14, 17, 21, 24, 26, and 27 are rejected under 35 U.S.C. §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. According to the Examiner, one of skill in the art would not be able to determine the scope of the presently claimed invention. Specifically, the phrase "wherein the characterization is conducted using mass spectrometry" is indefinite. Method steps should be recited as positive, active method steps. In addition, a question as to the limiting effect of the language in a claim is raised when "wherein" clauses are utilized. Furthermore, the fragmented, performed, derived, used, etc. of present claims 3, 4, 5, 6, and 26 should be written as positive, active method steps. All "using" or "used" limitations should be altered to "utilizing", etc. (see claims 1, 5, and 26). Furthermore, the claim limitation "those proteins, peptides, protein fragments, or peptide fragments binding to a specific antibody represent a heterogeneous class" is considered indefinite because the other limitations of method step (a) of claim 1 would lead one of skill in the art to believe that a single class is not heterogeneous, a single antibody would bind a relatively homogeneous group of proteins, peptides, protein fragments, or peptide fragments (i.e. antibody would bind to a specific motif common to all proteins, peptides, protein fragments, or peptide fragments that bind to the specific antibody). Moreover, according to the Examiner, it is not clear how "more than one protein, peptide, protein fragment, or peptide fragment" can bind to "each defined location on the array" (i.e. more than one protein, peptide, protein fragment, or peptide fragment binds to a single location on the array).

The Examiner has objected that the claims lack clarity for three reasons. Firstly, the Examiner has objected that the words "wherein", "using" and "used" are not positive method steps. Secondly, the Examiner has objected that the term "heterogeneous class" is unclear. Please delete the word "heterogeneous". The claims have been amended to address the points raised by the Examiner in her rejection of the claims.

Finally, the Examiner has objected that it is not clear how more than one protein, peptide, protein fragment or peptide fragment, can bind to each defined location on the array. It is clear from the specification that the defined location can comprise multiple copies of the same

antibody (see paragraph [0143]). Figures 2 to 14 also clearly show that multiple proteins of differing mass have been identified as bound to each particular ScFv. Hence, as there can be more than one copy of an antibody at any particular step, then more than one protein etc., can be captured. These proteins, peptides, protein fragments or peptide fragments, can be different providing they all share the same motif that is the specific target of the antibody.

In view of the above, Applicants respectfully request withdrawal of the rejections under §112, second paragraph.

**D. <u>The Claims Are Not Obvious in View of Minden, Nelson or Barry</u>**

Claims 1-11,13-14,17-18, 21, and 24-27 are rejected under 35 U.S.C. §103(a) as being unpatentable over Minden et al. WO 02/086081 A2 ("Minden") and Nelson et al. U.S. Patent 6,887,713 ("Nelson") and U.S. Patent Application Publication 2002/0110835 (published August 15, 2002; "Kumar".

Claims 1-11, 13-14, 17, 21, 24, and 26-27 are rejected under 35 U.S.C. 103(a) as being unpatentable over Minden et al. WO 02/086081 A2 (filing date April 22, 2002), Barry et al. WO 0225287 (filed September 19, 2001), and Kumar U.S. Patent Application Publication 2002/0110835 published August 15, 2002.

Applicant maintains that, for reasons detailed below, the present invention is not render obvious by Minden, Nelson, Kumar or Barry, either alone or in combination.

Applicants maintain that the array disclosed in Minden does not even resemble the array claimed in this application. The Minden array is an example of a format known as an antigen array (or reversed antibody array). In contrast, the claimed array is of the antibody array (forward array) type. These are completely different types of array as evidenced by the large number of publications in this area including the following references:

(i) Templin et al. (2003) Proteamics 3:2155-66 (Exhibit A) which discusses both reverse microarrays and standard protein microarrays (see contents and sections 2.1.1 and 2.3);

(ii) Wilson and Nock (2001) Curr Opin Chem Biol, 6:81-5 (Exhibit B) which discusses antibody arrays and reverse immunoarrays on page 83;

(iii) MacBeath (2002) Nat Genet. 32 suppl:526-32 (Exhibit C) which discusses antibody (antigen capture) and reverse (direct immunoarrays) throughout and is exemplified in figure 2;

(iv) Espina et al. (2003) Proteomics, 3:2091-2100 (Exhibit D) provides a review of microarrays and in section 2.1 discusses forward and reverse arrays;

(v) Poetz et al. (2005) Mech Ageing Dev. 126:161-170 (available online 20 October 2004) (Exhibit E) discusses in the introduction and shows in figure 1 that forward and reverse arrays are significantly different;

(vi) Wingren & Borrebeaeck (2006) OMICS 10:411-27 (Exhibit F); and

(vii) Wingren & Borrebaeck (2004) Expert Rev Proteomics 1:355-64 (Exhibit G) both provide a review of antibody arrays.

As can be seen from the attached documents, both before the priority date and in the art subsequently, the forward (antibody) and reverse (antigen) arrays were known to be different and have different functions. Addionally, the Examiner's attention is directed to Exhibit H, attached herewith demonstrating Minden's function in comparison to the technology encompassed by the claims of the present application.

Additionally, it should be noted that the claims have been amended to specify that the antibodies bind to greater than 2 different types of protein etc. The Examiner alleges that Minden discloses binding of motifs present in two or more different types of protein. However, Minden only describes (in Figures 4A-C) hypothetical proteins with epitopes in common. There is no substantiation of whether these hypothetical proteins are different proteins or whether they are merely variants of the same protein (and in which case would not be "different types"). Minden does not substantiate these in such a way that the skilled person would assume that a particular antibody would bind multiple proteins of different types. Conventionally, antibodies are understood to bind to a specific target and one skilled in the art would not expect one antibody to bind multiple proteins etc., that are conventionally unrelated (e.g., by function, 3D structure).

Furthermore, the Examiner alleges that Minden suggests that mass spectrometry is used and on this basis the Examiner believes it would be obvious to replace standard mass spectrometry with an alternative mass spectrometry version that measures both mass and abundance (e.g., MALDI-TOF). However, if Minden is read correctly, it does not disclose the use of any mass spectrometry. Paragraphs [0003] and [0004] of Minden which the Examiner relies upon actually teach that mass spectrometry is difficult, expensive and requires specialist skills to perform. In other words, Minden is directed to teaching other methods of reaching the same conclusion but without using mass spectrometry or variants thereof.

Applicants maintain that it is essential to note that the effect of the claimed array is to allow a significant reduction in the number of antibodies used for being able to analyse samples of large numbers of proteins, peptides, protein fragments or peptide fragements (including the entire proteome). This reduction is achieved by each antibody being capable of binding multiple different proteins, peptides, protein fragments or peptide fragements (that share a motif in common). The ability to bind multiple different proteins, peptides, protein fragments or peptide fragements sharing a motif is the essence of the invention and not how they are identified (i.e., the mass/abundance measurement step).

With regard to Nelson, Kumar and Barry, Applicant maintains that these references fail to supply the disclosure that is absent from Minden, i.e., a means for complex sample evaluation with relatively small arrays. The combined teachings of Minden and Nelson, Kumar and Barry, are conceptually different and not interchangeable with the claimed invention and would give strikingly different end results. Hence, the claims are non-obvious over the combination of Minden, Nelson, Kumar and Barry, therefore, the rejection under 35 U.S.C. §103 should be withdrawn.

Further, Applicants have added a new claim 50 which is directed to the number of antibodies present on the array being 150 or more. The number of antibodies being 150 or more is novel and non-obvious because Minden teaches that only 2-100 binding molecules can be used and paragraph [0073] in Minden suggests that 100 is the maximum that would work. Accordingly, having over 100 antibodies present would require inventive activity to get the array to work. Applicant maintains that none of the references cited by the Examiner, either alone or in combination, anticpate or render obvious the invention of claim 50.

## CONCLUSION

In view of the foregoing amendments and remarks, it is believed that the subject claims are in condition for allowance, which action is earnestly solicited. If, in the opinion of the Examiner, a telephone conference would expedite prosecution of the subject application, the Examiner is invited to call the undersigned attorney.

Respectfully submitted,

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